

Kling, L.L.; Leung, L.W.; Heng, H.H.; Isul, L.C.; Lassall, N.C.

Oncogene 9, 1745-1750, 1994
 A:Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domain
 A:Reference number: 158395; MUID:94239754; PMID:8183572
 A:Accession: 158395
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-847 <RES>
 A:Cross-references: GB:L32976; NID:9488295; PIDN:AAA59859.1; PID:9488296
 C:Genetics:
 A:Gene: GDB:MLK3; PTK1; SPRK
 A:Cross-references: GDB:134755; OMTM:600050
 A:Map position: 19q13.1-19q13.3
 C:Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
 C:Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein
 F:48-100/Domain: SH3 homology <SH3>
 F:115-383/Domain: protein kinase homology <KIN>
 F:123-131/Region: protein kinase ATP-binding motif
 F:403-424/Region: leucine zipper motif
 F:438-459/Region: leucine zipper motif
 F:468-482/Region: basic

Query Match 78.8%; Score 231; DB 1; Length 847;
 Best Local Similarity 77.8%; Pred. No. 1,6e-15;
 Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 HRDIKAGNILLLEKIEHDDCKNTKITDFGLAREHRTTKMSTAGTYAMAP 54
 DB 239 HRDIKSNILLLOPIESDMEHRTKITDFGLAREHRTTKMSTAGTYAMAP 292

RESULT 3

568178
 mixed-lineage protein kinase 2 (EC 2.7.1.1) - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
 C:Accession: 568178; 138044; S32468
 R:Dorow, D.S.; Devereux, L.; Tu, G.F.; Price, G.; Nicholl, J.K.; Sutherland, G.R.; Simps
 Eur. J. Biochem. 234, 492-500, 1995
 A:Title: Complete nucleotide sequence, expression, and chromosomal localization of human
 A:Reference number: 568178; MUID:96128179; PMID:8536694
 A:Accession: 568178
 A:Molecule type: mRNA
 A:Residues: 1-954 <DOR>
 A:Cross-references: EMBL:X90846; NID:9971419; PIDN:CAA62351.1; PID:9971420
 R:Katon, M.; Hirai, M.; Sugimura, T.; Terada, M.
 Oncogene 10, 1447-1451, 1995
 A:Title: Cloning and characterization of MST, a novel (putative) serine/threonine kinase
 A:Reference number: 138044; MUID:95249256; PMID:7731697
 A:Accession: 138044
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-461, 'A', 'V', 'A', 'S', 'A', '72-806, 'R', '808-817, 'A', '819-954 <RES>
 A:Cross-references: EMBL:Z48613; NID:9738592; PIDN:CA88531.1; PID:9738593
 R:Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
 Eur. J. Biochem. 213, 701-710, 1993
 A:Title: Identification of a new family of human epithelial protein kinases containing t
 A:Reference number: S32467; MUID:93238756; PMID:8477742
 A:Accession: S32468
 A:Molecule type: mRNA
 A:Residues: 244-464, 'AQAAGRRQHPQPALWL' <DOR>
 C:Genetics:
 A:Gene: GDB:MLK2; GDB:MSR
 A:Cross-references: GDB:362654; GDB:624810; OMTM:600137
 A:Map position: 19q13.1-19q13.2
 C:Superfamily: mixed-lineage protein kinase 2; protein kinase homology; SH3 homology
 C:Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein
 F:23-76/Domain: SH3 homology <SH3>
 F:96-364/Domain: protein kinase homology <KIN>
 F:104-112/Region: protein kinase ATP-binding motif
 F:384-405/Region: leucine zipper motif
 F:419-440/Region: leucine zipper motif
 F:449-463/Region: basic
 F:125,145,222,224/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 73.7%; Score 216; DB 1; Length 954;
 Best Local Similarity 72.2%; Pred. No. 5,7e-14;
 Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 1 HRDIKAGNILLLEKIEHDDCKNTKITDFGLAREHRTTKMSTAGTYAMAP 54
 DB 220 HRDIKSNILLLOPIESDMEHRTKITDFGLAREHRTTKMSTAGTYAMAP 273

RESULT 4

748206
 protein kinase ATN1-like protein - Arabidopsis thaliana
 N:Alternate names: protein T20L15.120
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
 C:Accession: 748206
 R:Bayan, M.; Peters, S.A.; van Staveren, M.; Dirksen, W.; Stiekema, W.; Bancroft, I.;
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: 748206
 A:Accession: 748206
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-356 <BEV>
 A:Cross-references: EMBL:AL162351
 A:Experimental source: cultivar Columbia; BAC clone T20L15
 C:Genetics:
 A:Map position: 5
 A:Introns: 170/1; 211/3; 264/3
 A:Note: T20L15.120
 C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 43.3%; Score 127; DB 2; Length 356;
 Best Local Similarity 51.8%; Pred. No. 1,6e-05;
 Matches 29; Conservative 7; Mismatches 10; Indels 10; Gaps 3;

OY 1 HRDIKAGNILLLEKIEHDDCKNTKITDFGLAREHRTTKMSTAGTYAMAP 54
 DB 164 HRDIKPNLLITLEN-----HRSVKLADFGIARE-ESVETMTAETGYRMVAP 211

RESULT 5

JC2363
 protein kinase (EC 2.7.1.37) ZPK - human
 N:Alternate names: leucine zipper protein kinase
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Feb-2001
 C:Accession: JC2363
 R:Reddy, U.R.; Pleasure, D.
 Biochem. Biophys. Res. Commun. 202, 613-620, 1994
 A:Title: Cloning of a novel putative protein kinase having a leucine zipper domain fr
 A:Reference number: JC2363; MUID:94311945; PMID:8037767
 A:Accession: JC2363
 A:Molecule type: mRNA
 A:Residues: 1-668 <RED>
 A:Cross-references: EMBL:U07358
 A:Experimental source: brain
 A:Note: the nucleotide sequence for this amino acid sequence is inconsistent with the
 he codon ACC for residue 661 as pro. the codon GAGCAGCTCTCA for residues 664-668 a
 C:Comment: This protein belongs to the family of non-receptor kinase.
 C:Genetics:
 A:Gene: GDB:ZPK
 A:Cross-references: GDB:383963; OMTM:600447
 A:Map position: 12q13-12q13
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
 C:Keywords: ATP; leucine zipper; nucleotide binding; P-loop; phosphotransferase
 F:123-371/Domain: protein kinase homology <KIN>
 F:131-139/Region: protein kinase ATP-binding motif
 F:443-471/Region: leucine zipper motif
 F:538-545/Region: nucleotide-binding motif A (P-loop)
 F:152/Active site: Lys #status predicted

Query Match 42.5%; Score 124.5; DB 2; Length 668;

hypothetical protein F25P22.8 [Imported] - Arabidopsis thaliana

A;Molecule type: DNA
A;Residues: 1-58 'T' 60-263 'D' 265-278 'T' 280-702 'S' 707-708 'KP' 714 'VTMTT' 715



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2
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